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; TOIG of: aj275971 check: 4487 from: 1 to: 1283
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; DEFINITION Gadus morhua mRNA for uracil-DNA glycosylase precursor (ung1 gene).
; ACCESSION AJ275971
; VERSION AJ275971.1 GI:7413911
; KEYWORDS precursor; ung1 gene; uracil-DNA glycosylase.
; SOURCE Atlantic cod.
; ORGANISM Gadus morhua
; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
; Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
; REFERENCE 1
; AUTHORS Lanes,O., Leiros,I., Smalas,A.O. and Willassen,N.P.
; TITLE Identification, cloning, and expression of uracil-DNA glycosylase from Atlantic cod (Gadus morhua): characterization and homology modeling of the cold-active catalytic domain
; JOURNAL Extremophiles 6 (1), 73-86 (2002)
; MEDLINE 21867342
; PUBMED 11878565
; REFERENCE 2 (bases 1 to 1283)
; AUTHORS Lanes,O.
; TITLE Direct Submission
; JOURNAL Submitted (02-MAR-2000) Lanes O., Department of Biotechnology, University of Tromsøe, Institute of Medical Biology, Medical Faculty, N-9037, NORWAY
; FEATURES
; source
; 1. 1283
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; VPPPSLVNIYKELCTDIDGFKHGHGDLGSKWAKQGVLLNVLTVRAHQANSKDRG
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; AJ275971 Length: 1283 June 17, 2003 08:47 Type: N Check: 4487
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; K.F.ARTLTPTVKHMSVCKSQFPLPVV.TYTKNCVPTLMASILDMEI.ADGKNGCCCLTRC.
; PCGPIPTPTREAGSPPTL.SSG.ASTGKEWFCSCGAHTPIRERPSGTGNVTMSCKLFIHLCLLIVG
; SLVSTSPRLTGC.NYLGRLS.TGEHNSLCLLITLVL.R.TSHYIFYSFKPIYKLSFVFWNDAAF
; RF.IKTLVHSAMLTHTVQSI.LSQLEQKCYFIIDYILYIKDCFPPLFPHY.DIKLLTYFP.CQLLKFL.
; CRNKLVI1
;
; AJ275971-pep.2
; TSACKYVQVRVMPKHHIIKSGLTRFTNSNFMFF.INEDNABETEVLKGTQDVATAFSAGKNGQK
; .ESSA.QD.SKNACRRRLDRKAGCRV.KAILQTIIDVICS..EESPLRPTG.SSVQDRDV.HSRCE
; SDRRPGPLRPSQPTWTLFQCAKSSPQVCKSQFPLPVV.TYTKNCVPTLMASILDMEI.ADGKNGCCCLTRC.
; RAGSGQLPQGRGLDHRCDVAERQSGFPVVGRLRP.EGSDHROETSPCLASCSISFVCSWV
; PML.ALLOQ.RAAETWDGAYKLESTLVAALVC.LF.DEHHTIFSTAFSSNOSTSPHLSFGMMLLV
; GERYLKHFTTLPCL.LMPSQYNHNLNKNVIL.LIIFCTKIVFPFGCFIGTRIILNCY.PIFHDVNCLSFY
; AEINYIF1
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; AJ275971-pep.3 frame 3
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; TOIG of: aj275972 check: 3502 from: 1 to: 1355
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; ACCESSION AJ275972
; VERSION AJ275972.1 GI:7413913
; KEYWORDS precursor; ung2 gene; uracil-DNA glycosylase.
; SOURCE Atlantic cod.
; ORGANISM Gadus morhua
; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
; Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
; REFERENCE 1
; AUTHORS Lanes,O., Leiros,I., Smalas,A.O. and Willassen,N.P.
; TITLE Identification, cloning, and expression of uracil-DNA glycosylase from Atlantic cod (Gadus morhua): characterization and homology modeling of the cold-active catalytic domain
; JOURNAL Extremophiles 6 (1), 73-86 (2002)
; MEDLINE 21867342
; PUBMED 11878565
; REFERENCE 2 (bases 1 to 1355)
; AUTHORS Lanes,O.
; TITLE Direct Submission
; JOURNAL Submitted (02-MAR-2000) Lanes O., Department of Biotechnology, University of Tromsøe, Institute of Medical Biology, Medical Faculty, N-9037, NORWAY
; FEATURES
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; VPPPSLVNIYKELCTDIDGFKHGHGDLGSKWAKQGVLLNVLTVRAHQANSKDRG
; WETFTDAVIKWLSVNRGVVFLWGSYAHKKGATIDRKRHHVLQAVHPSPLSAHRGFL
; GCKHFSKANGLLKLSGTEPINRAL"
; BASE COUNT 393 a 287 c 304 g 371 t
; ORIGIN
;
; AJ275972 Length: 1355 June 17, 2003 08:48 Type: N Check: 3502
; AJ275972-pep.1
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; AVTPTSLRIKCTVQRCVTFPKM.K.F.ARTLTPTVKHMSVCKSQFPLPVV.TYTKNCVPTLM
; SILDMEI.ADGKNGCCCLTRC.PCGPIPTPTREAGSPPTL.SSG.ASTGKEWFCSCGAHTPIRRE
; RPSGTGNVTMSCKLFIHLCLLIVGSLVSTSPRLTGC.NYLGRLS.TGEHNSLCLLITLVL.R.TSHYI
; FYSFKPIYKLSFVFWNDAAFGRF.IKTLVHSAMLTHTVQSI.LSQLEQKCYFIIDYILYIKDCFPFR
; LPHYR.DIKLLTYFP.CQLLKFLCRNKLVI1
;
; AJ275972-pep.2
; MV.EDSTLTIVSEGENGVIVHVLRLKNDWSTAYQLFLLTSFKKESFKGIR.NRKACRRSSDNABETE
; VLKCGTKDVATAFSAGKNGQK.ESSA.QD.SKNACRRRLDRKAGCRV.KAILQTIIDVICS..EE
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 STAFSSNQSI SFHLSFGMILLVGFYKHKHTTIPC.LMFSQYNFHNKNVIL.LIIFCTLKIVFFPG  
 CFIGTRILNCY.PIFHDVNCLSFYAEINIFI

AJ275972-pep\_3 *the frame 3*

WFRRIVL.HWLAQKTELLCISF.PYV.KMIGQOHINSFFSVSKRVSKELGKTEKHAEEVOITPKKL  
 SSNVEQKTSPLSVQELERMAKNKAALDKIRAKTAPAGGETWRRELAEEFEKPYFKQLMSFVADERS  
 RHTVYPADQVYSWTEMDIODVXVILGQDPYHGPNOAGLCSFVQKPPPPSLNIIYKELCTDIDGF  
 KHPGHDLGSAKQGVLLNNAVLTVRAHQANSHKORGWETFDVAVIKWLSVNRGCVFLLWGSYAHKKA  
 TIDRRHHVLQAVHPSPLSAHRGFLGCKHFKSANGLLKLSGTEPINMRAL.LFMLPYTVNCFKNNITLYF  
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 VS.VLGY.TVINLFSMMSTA.VFMQK.IIYI

IntelliGenetics,

# FastDB - Fast Pairwise Comparison of Sequences Release 5.4

Results file aj275971-pep\_3.res made by bobryen on Tue 17 Jun 103 9:10:30-PDT.

Query sequence being compared: AJ275971-pep\_3 (1-426)  
 Number of sequences searched: 6  
 Number of scores above cutoff: 6

Results of the initial comparison of AJ275971-pep\_3 (1-426) with:  
File : trans.pep

Item	Score
N	92
U	46
M	138
B	184
E	231
R	277
O	323
F	369
S	415
E	46
Q	138
U	184
U	231
E	277
N	323
C	369
E	415
S	46

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name	Description	Init. Opt.	Length	Score	Sig. Frame
...	...	...	...	...	...

1. AJ275971-pep\_3

The list of other best scores is:

Sequence Name	Description	Length	Score	Sig.	Frame
2. AJ275972-pep 3	*** 1 standard deviation above mean ***	436	375	392	1.19 0

1. AJ275971-pep\_3 (1-426)  
AJ275971-pep\_3

```
Initial Score      = 415 Optimized Score = 415 Significance = 1.39
Residue Identity  = 100% Matches      = 415 Mismatches = 0
Gaps              = 0 Conservative Substitutions = 0
```

X	10	20	30	40	50	60	70
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HPLANMLFKLGLCQRCISSNRVLPGLLIPOTLCFSKLMKTIPTPKLLRSSNEBQKTSPPQLSVQEQLERMAKNKK							
X	10	20	30	40	50	60	70
AALDKIRAKATPAGFGETWREIRLAAEFEPYFKQLMSFVADERSHITYVPADQVYSWTEMCIDIQVKVIL							
AALDKIRAKATPAGFGETWREIRLAAEFEPYFKQLMSFVADERSHITYVPADQVYSWTEMCIDIQVKVIL							
X	80	90	100	110	120	130	140
GODPYHGPNQAHGLCFSSQVQPPPSLVNIYKELCTDIDGFKPHGHGDLGSWAKQGVLLINAVLTVRAHQ							
GODPYHGPNQAHGLCFSSQVQPPPSLVNIYKELCTDIDGFKPHGHGDLGSWAKQGVLLINAVLTVRAHQ							
X	150	160	170	180	190	200	210
NSHKDRGWETFTDAVIKWLVSNRREGVVFLLMGSYAHKKGATIDRKHVHLQVAPHSPLSAHRGFLGCKHF							
NSHKDRGWETFTDAVIKWLVSNRREGVVFLLMGSYAHKKGATIDRKHVHLQVAPHSPLSAHRGFLGCKHF							
X	220	230	240	250	260	270	280
ANGLLKUSGTEPINNRALLFMLPYTNCFKMNTIYFLOLQVQVOTNLAFICLLSCCFMSVLDTNTPLCHVD							
ANGLLKUSGTEPINNRALLFMLPYTNCFKMNTIYFLOLQVQVOTNLAFICLLSCCFMSVLDTNTPLCHVD							
X	290	300	310	320	330	340	350
SCSVNITFTTTKMLFYNLYSVHRLFFPSQAVSVLGYVTINLFSMMSSTAVFMQKIY							
SCSVNITFTTTKMLFYNLYSVHRLFFPSQAVSVLGYVTINLFSMMSSTAVFMQKIY							
X	360	370	380	390	400	410	X
SCSVNITFTTTKMLFYNLYSVHRLFFPSQAVSVLGYVTINLFSMMSSTAVFMQKIY							
SCSVNITFTTTKMLFYNLYSVHRLFFPSQAVSVLGYVTINLFSMMSSTAVFMQKIY							

2. AJ275971-pep\_3 (1-426)  
AJ275972-pep\_3

```
Initial Score      = 375  Optimized Score = 392  Significance = 1.19
Residue Identity  = 91%  Matches      = 379  Mismatches = 34
Gaps              = 0    Conservative Substitutions = 2
```

72 AS275971 X 10 20 30 40 50  
 HPLANMLFKGLCORCISRRNVLPGLLPOTLCFCKMLKITPKLRRSSNVE  
 :  
 WFRRLVHLAKGTELLCISFPYKWIQQHINSFFPSVKRYSKELGTEKHAEEVOITPKLRRSSNVE  
 10 20 X 30 40 50 60 70  
 QKTSPPOLSVQELERMAKNKKAALDKIRAKATPAGFGETWRELAAEFEKPYFKOLMSFVADERSRHTVYPP  
 120  
 QKTSPPOLSVQELERMAKNKKAALDKIRAKATPAGFGETWRELAAEFEKPYFKOLMSFVADERSRHTVYPP

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      80      90      100      110      120      130      140
130      140      150      160      170      180      190
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150      160      170      180      190      200      210
ADQVYSWTENCDIQDKVWILGQDPYHGPNOAHGCLCFSVQKPPPPSLVNIYKELCTDIDGFKHPGHGDL
200      210      220      230      240      250      260
GWAQGVLLNNAVLTVRAHQANSHKDRGWETFTDAVIKWLVSNRGVVFLWGSYAHKKGATIDRKRHHVLQ
GWAQGVLLNNAVLTVRAHQANSHKDRGWETFTDAVIKWLVSNRGVVFLWGSYAHKKGATIDRKRHHVLQ
220      230      240      250      260      270      280
GWAQGVLLNNAVLTVRAHQANSHKDRGWETFTDAVIKWLVSNRGVVFLWGSYAHKKGATIDRKRHHVLQ
270      280      290      300      310      320      330
AVHPSPLSAHRGFLGCKHFSKANGLLKLSGTEPINWRALLFMLPYTVNCFKMNITLYFLQLFQVQTNLAFIC
AVHPSPLSAHRGFLGCKHFSKANGLLKLSGTEPINWRALLFMLPYTVNCFKMNITLYFLQLFQVQTNLAFIC
290      300      310      320      330      340      350      360
AVHPSPLSAHRGFLGCKHFSKANGLLKLSGTEPINWRALLFMLPYTVNCFKMNITLYFLQLFQVQTNLAFIC
340      350      360      370      380      390      400      410
LLECCFWSVLDNTLPLCHVDSCSVNITFTTTKMLFYNLYSVHRLFPFSQAVSVLGYTVINLFSMMSTAVFMQ
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370      380      390      400      410      420      430
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X
KIIY
KIIY
KIIY
X
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